

ALIGNMENT

LOCUS STMAFSAA 1203 bp DNA linear BCT 26-APR-1993
 DEFINITION S.griseus afsA gene encoding a possible A-factor biosynthesis protein.
 ACCESSION M24250
 VERSION M24250.1 GI:153148
 KEYWORDS A-factor biosynthesis.
 SOURCE Streptomyces griseus
 ORGANISM Streptomyces griseus
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
 REFERENCE 1 (bases 1 to 1203)
 AUTHORS Horinouchi, S., Suzuki, H., Nishiyama, M. and Beppu, T.
 TITLE Nucleotide sequence and transcriptional analysis of the Streptomyces griseus gene (afsA) responsible for A-factor biosynthesis
 JOURNAL J. Bacteriol. 171 (2), 1206-1210 (1989)
 COMMENT Original source text: S.griseus DNA.

Alignment Scores:

Pred. No.:	7.91e-56	Length:	1203
Score:	1050.50	Matches:	201
Percent Similarity:	73.57%	Conservative:	30
Best Local Similarity:	64.01%	Mismatches:	82
Query Match:	63.86%	Indels:	1
DB:	1	Gaps:	1

US-10-017-471B-17 (1-313) x STMAFSAA (1-1203)

Qy	1	MetProGluAlaValValLeuIleAsnSerAlaSerAspAlaAsnSerIleGluGlnThr	20
Db	165	ATGCCCAGAGCAGCAGTCTTGATCGATCCGGTGCCGACTATGGACGCGGAGGCCGAGGTG	224
Qy	21	AlaLeuProValProMetAlaLeuValHisArgThrArgValGlnAspAlaPheProVal	40
Db	225	GTGCATCCCGTGCGGATCGAGATGGTGACCCGACCGAGGCCGAGGACGCCTTTCCGCGC	284
Qy	41	SerTrpIleProLysGlyGlyAspArgPheSerValThrAlaValLeuProHisAspHis	60
Db	285	AACTGGGTACGCCTGGGGCGCGACCGGTTGCGGGTGAAGCGGTCCTTCCGCACGACCAT	344
Qy	61	ProPhePheAlaProValHisGlyAspArgHisAspProLeuLeuIleAlaGluThrLeu	80
Db	345	CCCTTCTTCGCTCCGGTGCGGTGACGACCTGCACGATCCGCTGCTGGTCCGCGAGGCCATG	404
Qy	81	ArgGlnAlaAlaMetLeuValPheHisAlaGlyTyrGlyValProValGlyTyrHisPhe	100
Db	405	CGGCAGGCGGCCATGCTCGCCTTCCACGCGGGTACGGGATCCCGCTCGGCTACCACTTC	464
Qy	101	LeuMetThr---LeuAspTyrThrCysHisLeuAspHisLeuGlyValSerGlyGluVal	119
Db	465	CTCCTGACGGAGCTGGACTACGTCTGCCATCCCGAGCACCTCGGCGTGGGGGGCGAGCCC	524
Qy	120	AlaGluLeuGluValGluValAlaCysSerGlnLeuLysPheArgGlyGlyGlnProVal	139
Db	525	ACCGAGATCGGCCTGGAGGTGTTCTGCTCCGACCTGAAGTGGCGGGCCGGGCTCCCGGCG	584

Qy	140	GlnGlyGlnValAspTrpAlaValArgArgAlaGlyArgLeuAlaAlaThrGlyThrAla	159
		:::	
Db	585	CAGGGGCGCGTCGGCTGGGCGGTGCACCGGGGCGACCGGCTCGCCGCGACGGGGGTGGCG	644
Qy	160	ThrThrArgPheThrSerProGlnValTyrArgArgMetArgGlyAspPheAlaThrPro	179
		:	
Db	645	GCGACCCGGTTCAGCACGCCCAAGGCCCTACCGGCGGATGCGCGGTGACGTCCCGGTCGAG	704
Qy	180	ThrAlaSerValProGlyThrAlaProValProAlaAlaArgAlaGlyArgThrArgAsp	199
		:::	
Db	705	GGCATATCCCTACCGGAGACCGCGCCGGTCCCGGCCCTCGCCGGCGGGCCGCGCCCGCGTC	764
Qy	200	GluAspValValLeuSerAlaSerSerGlnGlnAspThrTrpArgLeuArgValAspThr	219
Db	765	GAGGACGTGGTGCTCTCGGGGACGGGGCGGGAGGGAGTCTGGGAAGTGC GCGTGGACACC	824
Qy	220	SerHisProThrLeuPheGlnArgProAsnAspHisValProGlyMetLeuLeuLeuGlu	239
Db	825	CGGCATCCGACCCTCTTCCAGCGCCCCAACGACCACGTCCCGGGCATGCTCCTGCTGGAG	884
Qy	240	AlaAlaArgGlnAlaAlaCysLeuValThrGlyProAlaProPheValProSerIleGly	259
Db	885	GCGGCCCGTCAGGCCGCGTGCCTGGTGGCGGGGCCCCGCGGAATCGTTCGGTGGAGGCG	944
Qy	260	GlyThrArgPheValArgTyrAlaGluPheAspSerProCysTrpIleGlnAlaThrVal	279
Db	945	CGCACCCGGTTCACCGGTACTCCGAGTTCGGCAGCCCGTGCTGGATAGGGGCGGTGGTC	1004
Qy	280	ArgProGlyProAlaAlaGlyLeuThrThrValArgValThrGlyHisGlnAspGlySer	299
		:::	
Db	1005	CAGCCGGGGGCGGACGAGGATACGGTGACCGTCCGGGTGACAGGCCATCAGGACGGCGAG	1064
Qy	300	LeuValPheLeuThrThrLeuSerGlyProAlaPheSerGly	313
Db	1065	ACGGTCTTCTCCACGGTCTGTCCGGCCCCCGGGCCACGGC	1106

LOCUS AB001608 1215 bp DNA linear BCT 22-NOV-1997
 DEFINITION Streptomyces virginiae DNA for BarX, complete cds.
 ACCESSION AB001608
 VERSION AB001608.1 GI:2641955
 KEYWORDS BarX.
 SOURCE Streptomyces virginiae
 ORGANISM Streptomyces virginiae
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 Streptomycineae; Streptomycetaceae; Streptomyces.
 REFERENCE 1 (sites)
 AUTHORS Kinoshita,H., Ipposhi,H., Okamoto,S., Nakano,H., Nihira,T. and Yamada,Y.
 TITLE Butyrolactone autoregulator receptor protein (BarA) as a transcriptional regulator in Streptomyces virginiae
 JOURNAL J. Bacteriol. 179 (22), 6986-6993 (1997)
 REFERENCE 2 (bases 1 to 1215)
 AUTHORS Kinoshita,H.
 TITLE Direct Submission
 JOURNAL Submitted (06-MAR-1997) Hiroshi Kinoshita, Osaka University, Department of Engineering; Yamadaoka 2-1, Suita, Osaka 565, Japan (E-mail:kinosita@biochem.bio.eng.osaka-u.ac.jp, Tel:+81-6-879-7433, Fax:+81-6-879-7432)

Alignment Scores:

Pred. No.:	5.99e-26	Length:	1215
Score:	562.50	Matches:	126
Percent Similarity:	56.12%	Conservative:	39
Best Local Similarity:	42.86%	Mismatches:	118
Query Match:	34.19%	Indels:	11
DB:	1	Gaps:	3

US-10-017-471B-17 (1-313) x AB001608 (1-1215)

Qy	19	GlnThrAlaLeuPro-----ValProMetAlaLeuVal	29
Db	214	CAGACCGGCCGACCGGCCCGCGCATCGGCCATGACCAGCACGGTTCGCGGGAGCTGGTC	273
Qy	30	HisArgThrArgValGlnAspAlaPheProValSerTrpIleProLysGlyGlyAspArg	49
		:: ::	
Db	274	CACCGGGCGCGGTCGCCGAAGTGTCTGACGGGATGGAGCCGACCGCGGAGAACCGA	333
Qy	50	PheSerValThrAlaValLeuProHisAspHisProPhePheAlaProValHisGlyAsp	69
		::: :: ::	
Db	334	TTCGCCCTGACGGCGCAGTGGCCCAGGGCGCACAGCTACTTCACCCCGGTGAACGGC---	390
Qy	70	ArgHisAspProLeuLeuIleAlaGluThrLeuArgGlnAlaAlaMetLeuValPheHis	89
		::: :: ::: ::	
Db	391	TGCTACGACCCGCTGCTGGCCTCCGAAACCATCCGACAGGTTCGGTACCCTTCTCTCCAC	450
Qy	90	AlaGlyTyrGlyValProValGlyTyrHisPheLeuMet---ThrLeuAspTyrThrCys	108
		::: :::::	
Db	451	GCGGAGTTCGGGGTCTCGTTCGGGGACAGTTCCTGATGTGGGACCTTCACCACAGCGTC	510
Qy	109	HisLeuAspHisLeuGlyValSerGlyGluValAlaGluLeuGluValGluValAlaCys	128
		::: ::: :::	
Db	511	AGGCCCCGAGCAGGCGGGCGTTCGGTCCCGCCCGGCGGACCTGGAAGTGGACGTCATCTGT	570

Qy		129 SerGlnLeuLysPheArgGlyGlyGlnProValGlnGlyGlnValAspTrpAlaValArg	148
		::::: ::: :~: ~: :~:	
Db		571 TCCGACATCCGCCCGCCGGCCGCCTGGCGGGCATGCGCTACGAGGTACCCTCTAC	630
Qy		149 ArgAlaGlyArgLeuAlaAlaThrGlyThrAlaThrThrArgPheThrSerProGlnVal	168
		::::: ~~~~~ ~~~~~	
Db		631 TGCGGGCGCCAGGTGATCGCCACCGGGCGGCCGCCCTTCGACTGCACCAGCCCCGCCGTC	690
Qy		169 TyrArgArgMetArgGlyAspPheAlaThrProThrAlaSerValProGlyThrAlaPro	188
		::~: :::: ~~~~~ ~~~	
Db		691 TACCAGCGGCTGCGCGGTGACCGGGTGGTGCCACGGGCGTGCGGCCCTGCCGCAGCCG	750
Qy		189 ValProAlaAlaArgAlaGlyArgThrArgAspGluAspValValLeuSerAlaSerSer	208
		::~: ~: ~~~~~ ~~~~~ ~~~~~ ~~~~~ ::~:	
Db		751 CTCGCCCCCGCGTCGGTCGGCCGCTTCCTCACCACGGACGTCGTCCTGTCCGCCACCGAG	810
Qy		209 GlnGlnAspThrTrpArgLeuArgValAspThrSerHisProThrLeuPheGlnArgPro	228
		::~: ::~ ~~~~~ ~~~~~ ~~~~~	
Db		811 CGTCCGCTGGAGTTGGCAGCTGCGGGTGGACGAACAGCATCCCCTGCTCTTCGACCACCTT	870
Qy		229 AsnAspHisValProGlyMetLeuLeuLeuGluAlaAlaArgGlnAlaAlaCysLeuVal	248
		~~~~~   ~~~~~  ::~:   ~: ::~:   ~: ::~:  ~~~~~  ::~:	
Db		871 GTCGACCACGTTCCCGGCATGGTGCTGATGGAGTCCGCCCCCAGGCCGCCAGGCCATC	930
Qy		249 ThrGlyProAlaProPheValProSerIleGlyGlyThrArgPheValArgTyrAlaGlu	268
		~~~~~  ::~:   ~: ::~:   ~:  ~~~~~	
Db		931 GACCCGTCCTCGGCCGTTCTCTGCCGACCACGATGCGCTCCGAGTTCAGCCGGTACGCGGAG	990
Qy		269 PheAspSerProCysTrpIleGlnAlaThrValArgProGlyProAlaAlaGlyLeuThr	288
		~: ~~~~~ ~~~~~ ~: ~~~~~	
Db		991 CTCGACAGGCCCTGCTGGATAACAGGCGGAGCCGCTGCCCGCGGCCGACAACGGCGACCGG	1050
Qy		289 ThrValArgValThrGlyHisGlnAspGlySerLeuValPhe	302
		~~~~~   ~~~~~  ::~:  ~~~~~	
Db		1051 CAGGTCCGCGTCAACGGCCACCAGGACGACACCACCGTCTTC	1092